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SEQUENCE LISTING

#6

> DING, SHI-YOU
ADNEY, WILLIAM S.
VINZANT, TODD B.
DECKER, STEPHEN R.
HIMMEL, MICHAEL E.

<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
CELLULOLYTICUS

<130> 40170.6US01

<140> 09/917,383
<141> 2001-07-28

<160> 14

<170> PatentIn Ver. 2.1

<210> 1
<211> 1228
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Segment of
GuxA

<400> 1
Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala
50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala
65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp
130 135 140

TECH CENTER 1600/2900

JAN 14 2002

RECEIVED

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro
 145 150 155 160
 Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro
 165 170 175
 Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val
 180 185 190
 Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser
 195 200 205
 Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu
 210 215 220
 Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met
 225 230 235 240
 Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly
 245 250 255
 Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn
 260 265 270
 Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys
 275 280 285
 Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu
 290 295 300
 Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr
 305 310 315 320
 Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser
 325 330 335
 Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn
 340 345 350
 Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn
 355 360 365
 Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln
 370 375 380
 Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe
 385 390 395 400
 Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu
 405 410 415
 Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser
 420 425 430
 Asp Pro Met Cys Asp Pro Thr Tyr Thr Ser Tyr Gly Val Leu Thr
 435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln
450 455 460

Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr
465 470 475 480

Ser Ser Ser Pro Pro Pro Pro Pro Ser Pro Ser Ala Ser Pro Ser
485 490 495

Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser
500 505 510

Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
515 520 525

Ser Ser Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser
530 535 540

Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser
545 550 555 560

Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Pro Ser
565 570 575

Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr
580 585 590

Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu
595 600 605

Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr
610 615 620

Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr
625 630 635 640

Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe
645 650 655

Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu
660 665 670

Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile
675 680 685

Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn
690 695 700

Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val
705 710 715 720

Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly
725 730 735

Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val
 755 760 765

Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr
 770 775 780

Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu
 785 790 795 800

Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala
 805 810 815

Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn
 820 825 830

Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Ser Pro Ser
 835 840 845

Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly
 850 855 860

Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val
 865 870 875 880

Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn
 885 890 895

Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly
 900 905 910

Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His
 915 920 925

Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser
 930 935 940

Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser
 945 950 955 960

Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr
 965 970 975

Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser
 980 985 990

Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr
 995 1000 1005

Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp
 1010 1015 1020

Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn
 1025 1030 1035 1040

Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu
 1045 1050 1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp
 1060 1065 1070

Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr
 1075 1080 1085

Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro
 1090 1095 1100

Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro
 1105 1110 1115 1120

Thr Ser Ser Pro Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val
 1125 1130 1135

Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr
 1140 1145 1150

Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe
 1155 1160 1165

Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln
 1170 1175 1180

Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile
 1185 1190 1195 1200

Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly
 1205 1210 1215

Thr Asn Ala Ala Pro Thr Leu Ser Cys Thr Ala Ser
 1220 1225

<210> 2
 <211> 3687
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Segment of
 GuxA

<400> 2
 atggagcgaa cccaaacaatc cggacggaac tgcaggtacc agagaggaac gacacgaatg 60
 cccgcacatct caaaaacggct gcgagccggc gtcctcgccg gggcggtgag catcgacgac 120
 tccatcgatcg cgcgtggcgat gcagcatcct gccatcgccg cgacgcacgt cgacaatccc 180
 tatgcgggag cgacccttctt cgtcaaccccg tactggcgcc aagaagtaca gagcgaagcg 240
 gcgaaaccaga ccaatgccac tctcgacgcg aaaaatgcgcg tcgttccac atattcgacg 300
 gccgtcttgg a tggaccgcattt cgctgcgcattt aacggcgatca acggcgacc cggcttgacg 360
 acatatctgg acggccgcctt ctcccacgcg caggaaaccatcccttgaatgtt cattgagatt 420
 gtcatctacg atctgcggg acgcgactgc gcgccgcctt cttccaaacgg cgaactgccc 480
 gctacggcag caggtttgca gacctatgaa acgcgactaca tcgatccatgcgagtttgc 540
 ctgagcaatc cgaagtttttgcgatc cagcctgcgg atcgtgcgcgatc tcattggatcc ggactcgctg 600
 ccaaacgcgg tcaccaatat gaggatccaa gctgtgcggatccggcggtgccc gtattacgatg 660
 caaggcatcg agtacgcgcctt cacgaaatttgc cacgcccattt cgaacgtgtatcatctatcg 720
 gacgcccggcc actccggcttgc gcttgggtgg cccaaataatgc ccagcggata cgtacaggaa 780
 gtccagaagg tcctcaacgc gaggatcggttgc gtcacacggca tcgacggctt cgtcaccaac 840

acggcgaatt acacgcccgtt gaaggagccg ttcatgacccg ccacccagca ggtcggcgga 900
 cagccgggtgg agtcggcgaa tttctaccag tggaatccctg acatcgacga agccgactac 960
 gcggttgact tgtactcgcg gtcgtcgcc gctggcttcc caagcagcat cggcatgttc 1020
 atcgacacct tacgcaacgg ttgggggtgg csgaacaacaa caacaggccc gacgaccggcg 1080
 accgatgtca acacccgttca aacccagtcg aagattgacc ttcggcagca cccggggctg 1140
 tggtgcaacc agaacgggtgc gggcctcgcc cagccgccc aggcaagccc gacggacttc 1200
 csgaacaacgc acctcgacgc gtatgtctgg atcaagccgc cgggtgagtc ggacggcaca 1260
 agcgctgcga gcgatccgac aactgcaag aagtccggacc ccatgtgcga cccgacgtac 1320
 acgacgttgt acgggggtact gaccaacgcg ttaccgaact ccccgatcgc cggccagtgg 1380
 ttcccggcgc agtttgacca gcttgcgcg aacgcacggc cagccgtgcc gacgtcgacc 1440
 agctcgagcc cggccgttcc gccgcccgtt cggcgtggctt cggcgttcc gagcccgagt 1500
 csgagcccgaa gcaagtcgcg atcggcgtcg cggcgttccca gtcgagcccc gtctccgtcg 1560
 csgagcccgaa gttccgagccc gatgtactcg cggcgtccgt ctccgagctc gagcccgct 1620
 cggcgtcccgaa gcccggatcc gagcccgagt agctcgccgt cggcgttcc gagctcgagc 1680
 cggcgttccgt cggcggagccc gatgtcgac cggagtagct cggcgttccca gtctccgacg 1740
 tggcgtcccgaa tgggggtgg gctgaagggtt cagtagacaaga acaatgattt ggccgggggt 1800
 gataaccaga tcaaaccggg tctccagttt gtgaataacccg ggtcgtcgac ggtggattt 1860
 tcgacgggtga cgggtcggttta ctgggttccacc cgggatgggtt ggtcgtcgac actgggttac 1920
 aactgtgact gggccggcgat ggggtgtggg aatatcccgcc ctcgttccgg ctcggtaac 1980
 cccggcgcacgc cgaacggcgaa cacctacccgt cagttgtcg tcaactgggtt aacgttggcc 2040
 gttgggtggg cgaacgggtga gattcaaaac cgggtgaata agagtgactg gtcgaattt 2100
 accgagacca atgactactc gtatgggacg aacaccaccc tccaggactg gacgaaggtg 2160
 acgggtgtacg tcaacggcgat gttgggtgtgg gggactgaac cgtccggcac cagcccccagc 2220
 cccacacccat ccccgagccc gagcccgagc cggagccccgg gttgggtatgt gacgcccggc 2280
 agtgtgcgaa cccggcttggg ggtgacgggg gtgagttggg cgtcgggtgc gttgggtgg 2340
 aatcgctcgaa cggataaacgt ggggggtggcg cattacaacg tgcgttccaa cgggggtttt 2400
 gtggggccagc cgaacgggtac ctcgttccacc gacacgggtt tggccggggg aaccgcgtac 2460
 acctacacccg tggccggcggt ggacgctcg ggttaacaccc cccgccccatc cccccccgtc 2520
 accggccacca ccacgagtc cagcccccagc cccacggccg cgggaccac ggtcaccgac 2580
 tgcacgccccg gtccctaaacca gaatgggtgtt accagcgtgc agggcgacga ataccgggt 2640
 cagaccaatg agtggaaattt gtcggcccgag cagtcgttccca ccatcaatac cgcgaccgg 2700
 gcttggacgg tgagcactgc gaacttcagc ggtggggaccg gcggtgcgc cgcgacgtat 2760
 cccgtcgatct acaagggctg ccactggggc aactgcacca cgaagaacgt cgggatggcc 2820
 attcagatca gtcagattgg ttcgggtgtt acgtcggttgg gtaacgcac ggtgtcg 2880
 ggcgcgtatg acgtggccta cgaacattgg acgaacagata ccccaacgc aaccggtcag 2940
 ccaaacggta cggaaatcat gatttggctg aattcgctg gttgggtgca gccgttccgg 3000
 tcgcagacacg cgaacgggtgt gacgggtcgct ggtcacacgt ggaatgtctg gcagggtcag 3060
 cagacccgtt ggaagattt ttcctacgtc ctgacccccc gtcgacgtc gatcagtaat 3120
 ctggatttta aggcgatttt cgcggacgc cggcgcacgc ggtcgctcaa cacctccgt 3180
 tacctgtctcg acgttgaggc cgggttttagt atctggcaag gtggtcaggg cctggggcagc 3240
 aactcggtca gctgtccgt gacgagccgc acgtccagcc cgcacccgg cccgagcccg 3300
 acggccgacac cggacccggc gcccacaccg tcccgagcc cgcacccgtc gccgagtcgg 3360
 accagctcgcc cgtcgtcgcc ggggtgtggcg tgccggggca cgtatgtggt gaatagtgtat 3420
 tgggggttctg ggtttacggc gacgggtgacg gtgacgaaata cgggagccg ggcgacgaac 3480
 ggggtggacgg tggcgtggc gtttgggtgg aatcagacgg tcacgaacta ctggaaact 3540
 gcggtgaccc aatcaggtgc atcggtgacg gcgacgaacc tgagttacaa caacgtgatc 3600
 caaccgggtc agtcgaccac cttcggttcc aacggaaatgt actcaggaac aaacgcccgg 3660
 cccgacgtca gtcgacacgc cagctg 3687

<210> 3
 <211> 53
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Segment of
 GuxA

<400> 3

Met	Glu	Arg	Thr	Gln	Gln	Ser	Gly	Arg	Asn	Cys	Arg	Tyr	Gln	Arg	Gly
1				5				10				15			

Thr	Thr	Arg	Met	Pro	Ala	Ile	Ser	Lys	Arg	Leu	Arg	Ala	Gly	Val	Leu
			20					25				30			

Ala	Gly	Ala	Val	Ser	Ile	Ala	Ala	Ser	Ile	Val	Pro	Leu	Ala	Met	Gln
			35				40				45				

His	Pro	Ala	Ile	Ala											
			50												

<210> 4

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 4

Ala	Thr	His	Val	Asp	Asn	Pro	Tyr	Ala	Gly	Ala	Thr	Phe	Phe	Val	Asn
1			5					10				15			

Pro	Tyr	Trp	Ala	Gln	Glu	Val	Gln	Ser	Glu	Ala	Ala	Asn	Gln	Thr	Asn
			20				25				30				

Ala	Thr	Leu	Ala	Ala	Lys	Met	Arg	Val	Val	Ser	Thr	Tyr	Ser	Thr	Ala
			35				40			45					

Val	Trp	Met	Asp	Arg	Ile	Ala	Ala	Ile	Asn	Gly	Val	Asn	Gly	Gly	Pro
		50				55			60						

Gly	Leu	Thr	Thr	Tyr	Leu	Asp	Ala	Ala	Leu	Ser	Gln	Gln	Gly	Thr	
65					70				75			80			

Thr	Pro	Glu	Val	Ile	Glu	Ile	Val	Ile	Tyr	Asp	Leu	Pro	Gly	Arg	Asp
			85				90		95						

Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Leu	Pro	Ala	Thr	Ala	Ala	Gly
			100				105			110					

Leu	Gln	Thr	Tyr	Glu	Thr	Gln	Tyr	Ile	Asp	Pro	Ile	Ala	Ser	Ile	Leu
115					120			125							

Ser	Asn	Pro	Lys	Tyr	Ser	Ser	Leu	Arg	Ile	Val	Thr	Ile	Ile	Glu	Pro
	130					135			140						

Asp	Ser	Leu	Pro	Asn	Ala	Val	Thr	Asn	Met	Ser	Ile	Gln	Ala	Cys	Ala
145				150				155			160				

Thr	Ala	Val	Pro	Tyr	Tyr	Glu	Gln	Gly	Ile	Glu	Tyr	Ala	Leu	Thr	Lys
			165				170		175						

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
 180 185 190
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
 195 200 205
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
 210 215 220
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
 225 230 235 240
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
 245 250 255
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
 260 265 270
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
 275 280 285
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
 290 295 300
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
 305 310 315 320
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
 325 330 335
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
 340 345 350
 Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
 355 360 365
 Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
 370 375 380
 Pro Thr Tyr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
 385 390 395 400
 Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
 405 410 415
 Ala Asn Ala Arg Pro Ala Val
 420

<210> 5
 <211> 150
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Segment of
 GuxA

<400> 5
 Val Ser Gly Gly Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro
 1 5 10 15
 Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser
 20 25 30
 Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
 35 40 45
 Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
 50 55 60
 Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
 65 70 75 80
 Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu
 85 90 95
 Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser
 100 105 110
 Asp Trp Ser Asn Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn
 115 120 125
 Thr Thr Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val
 130 135 140
 Leu Val Trp Gly Thr Glu
 145 150

<210> 6
 <211> 1043
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Segment of
 GuxA

<400> 6
 Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
 1 5 10 15
 Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
 20 25 30
 Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
 35 40 45
 His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala
 50 55 60
 Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala
 65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser
 85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly
 100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser
 115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp
 130 135 140

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro
 145 150 155 160

Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro
 165 170 175

Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val
 180 185 190

Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser
 195 200 205

Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu
 210 215 220

Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met
 225 230 235 240

Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly
 245 250 255

Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn
 260 265 270

Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys
 275 280 285

Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu
 290 295 300

Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr
 305 310 315 320

Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser
 325 330 335

Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn
 340 345 350

Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn
 355 360 365

Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln
 370 375 380

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe
 385 390 395 400

Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu
 405 410 415

Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser
 420 425 430

Asp Pro Met Cys Asp Pro Thr Tyr Thr Ser Tyr Gly Val Leu Thr
 435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln
 450 455 460

Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Val Ser Gly Gly
 465 470 475 480

Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln
 485 490 495

Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp
 500 505 510

Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser
 515 520 525

Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn
 530 535 540

Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp
 545 550 555 560

Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly
 565 570 575

Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn
 580 585 590

Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln
 595 600 605

Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly
 610 615 620

Thr Glu Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val Thr
 625 630 635 640

Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr Asp
 645 650 655

Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val
 660 665 670

Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly
 675 680 685

Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr
 690 695 700

Ser Ala Pro Ser Thr Pro Val Asp Cys Thr Pro Gly Pro Asn Gln Asn
 705 710 715 720

Gly Val Thr Ser Val Gln Asp Gly Glu Tyr Arg Val Gln Thr Asn Glu
 725 730 735

Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn Thr Ala Thr Gly
 740 745 750

Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly Thr Gly Gly Ala
 755 760 765

Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His Trp Gly Asn Cys
 770 775 780

Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser Gln Ile Gly Ser
 785 790 795 800

Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser Gly Ala Tyr Asp
 805 810 815

Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr Thr Gly Gln
 820 825 830

Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser Arg Gly Gly Val
 835 840 845

Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr Val Ala Gly His
 850 855 860

Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp Lys Ile Ile Ser
 865 870 875 880

Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn Leu Asp Leu Lys
 885 890 895

Ala Ile Phe Ala Asp Ala Ala Arg Gly Ser Leu Asn Thr Ser Asp
 900 905 910

Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp Gln Gly Gly Gln
 915 920 925

Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr Ser Gly Gly Val
 930 935 940

Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser Gly Phe
 945 950 955 960

Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr Asn Gly
 965 970 975

Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr Asn Tyr
 980 985 990

Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala Thr Asn
 995 1000 1005

Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr Phe Gly
 1010 1015 1020

Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu Ser Cys
 1025 1030 1035 1040

Thr Ala Ser

<210> 7

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
 GuxA

<400> 7

Asp Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Asp
 1 5 10 15

Gly Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln
 20 25 30

Cys Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala
 35 40 45

Asn Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile
 50 55 60

Tyr Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met
 65 70 75 80

Pro Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr
 85 90 95

Thr Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr
 100 105 110

Asn Ser Thr Pro Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met
 115 120 125

Ile Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr
 130 135 140

Ala Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly
 145 150 155 160

Gln Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala
 165 170 175

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala
 180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala
 195 200 205

Gly Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe
 210 215 220

Ser Val Ser Val Thr Ser Gly
 225 230

<210> 8

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
 GuxA

<400> 8

Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser
 1 5 10 15

Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr
 20 25 30

Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr
 35 40 45

Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala
 50 55 60

Thr Asn Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr
 65 70 75 80

Phe-Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu
 85 90 95

Ser Cys Thr Ala Ser
 100

<210> 9

<211> 423

<212> PRT

<213> Acidothermus cellulolyticus

<400> 9

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn
 1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn
 20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro
 50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr
 65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp
 85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly
 100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu
 115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro
 130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala
 145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys
 165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
 180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
 195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
 210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
 225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
 245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
 260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
 275 280 285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
 290 295 300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
 305 310 315 320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
 325 330 335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
 340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
 355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
 370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
 385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
 405 410 415

Ala Asn Ala Arg Pro Ala Val
 420

<210> 10
 <211> 430
 <212> PRT
 <213> Cellulomonas fimi

<400> 10
 Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val
 1 5 10 15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Gly Arg Gln Ser
 20 25 30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro
 35 40 45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp
 50 55 60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys
 65 70 75 80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro
 85 90 95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr
 100 105 110

Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala
 115 120 125

Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr
 130 135 140

Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro
 145 150 155 160

Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala
 165 170 175

Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile
 180 185 190

Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala
 195 200 205

Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser
 210 215 220

Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu
 225 230 235 240

Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg
 245 250 255

Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr
 260 265 270

Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser
 275 280 285

Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn
 290 295 300

Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp
 305 310 315 320

Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro
 325 330 335

Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr
 340 345 350

Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu
 355 360 365

Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe
 370 375 380

Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln
 385 390 395 400

Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu
 405 410 415

Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile
 420 425 430

<210> 11
 <211> 432
 <212> PRT
 <213> Thermobifida fusca

<400> 11
 Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp
 1 5 10 15

Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala
 20 25 30

Lys Ala Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr
 35 40 45

Ala Val Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro
 50 55 60

Thr Thr Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg
 65 70 75 80

Gln Ser Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu
 85 90 95

Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro
 100 105 110

Asp Glu Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp
 115 120 125

Ile Met Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile
 130 135 140

Ile Glu Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn
 145 150 155 160

Gly Gly Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val
 165 170 175

Asn Gly Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val
 180 185 190

Tyr Asn Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser
 195 200 205

Asn Phe Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser
 210 215 220

Gly Ser Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn
 225 230 235 240

Tyr Ser Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn
 245 250 255

Gly Gln Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val
 260 265 270

Asp Glu Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys
 275 280 285

Gly Phe Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly
 290 295 300

Trp Gly Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu
 305 310 315 320

Asn Thr Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly
 325 330 335

Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val
 340 345 350
 Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly
 355 360 365
 Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly
 370 375 380
 Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly
 385 390 395 400
 Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp
 405 410 415
 Phe Ser Ala Gln Phe Arg Glu Leu Ala Asn Ala Tyr Pro Pro Leu
 420 425 430

<210> 12
 <211> 221
 <212> PRT
 <213> Acidothermus cellulolyticus

<400> 12
 Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg
 1 5 10 15
 Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile
 20 25 30
 Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val
 35 40 45
 Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys
 50 55 60
 His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser
 65 70 75 80
 Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn
 85 90 95
 Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg
 100 105 110
 Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val
 115 120 125
 Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly
 130 135 140
 Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val
 145 150 155 160

Ile Ser Phe Leu Ala Pro Ser Ala Ile Ser Ser Trp Ser Phe Asp Val
 165 170 175

Lys Asp Phe Val Asp Gln Ala Val Ser His Gly Leu Ala Thr Pro Asp
 180 185 190

Trp Tyr Leu Thr Ser Ile Gln Ala Gly Phe Glu Pro Trp Glu Gly Gly
 195 200 205

Thr Gly Leu Ala Val Asn Ser Phe Ser Ser Ala Val Asn
 210 215 220

<210> 13

<211> 221

<212> PRT

<213> Streptomyces sp.

<400> 13

Asp Thr Thr Ile Cys Glu Pro Phe Gly Thr Thr Thr Ile Gln Gly Arg
 1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Ser Thr Ala Pro Gln Cys Val
 20 25 30

Thr Ala Thr Asp Thr Gly Phe Arg Val Thr Gln Ala Asp Gly Ser Ala
 35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Phe Asn Gly Cys
 50 55 60

His Tyr Thr Asn Cys Ser Pro Gly Thr Asp Leu Pro Val Arg Leu Asp
 65 70 75 80

Thr Val Ser Ala Ala Pro Ser Ser Ile Ser Tyr Gly Phe Val Asp Gly
 85 90 95

Ala Val Tyr Asn Ala Ser Tyr Asp Ile Trp Leu Asp Pro Thr Ala Arg
 100 105 110

Thr Asp Gly Val Asn Gln Thr Glu Ile Met Ile Trp Phe Asn Arg Val
 115 120 125

Gly Pro Ile Gln Pro Ile Gly Ser Pro Val Gly Thr Ala Ser Val Gly
 130 135 140

Gly Arg Thr Trp Glu Val Trp Ser Gly Gly Asn Gly Ser Asn Asp Val
 145 150 155 160

Leu Ser Phe Val Ala Pro Ser Ala Ile Ser Gly Trp Ser Phe Asp Val
 165 170 175

Met Asp Phe Val Arg Ala Thr Val Ala Arg Gly Leu Ala Glu Asn Asp
 180 185 190

Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly
 195 200 205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu
 210 215 220

<210> 14
 <211> 228
 <212> PRT
 <213> Streptomyces lividans

<400> 14
 Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp
 1 5 10 15

Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys
 20 25 30

Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn
 35 40 45

Phe Ser Gly Gly Thr Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr
 50 55 60

Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro
 65 70 75 80

Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr
 85 90 95

Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn
 100 105 110

Ser Thr Pro Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile
 115 120 125

Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala
 130 135 140

Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln
 145 150 155 160

Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr
 165 170 175

Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala
 180 185 190

Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly
 195 200 205

Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser
 210 215 220

Val Ser Val Thr
 225